

## SEQUENCE LISTING

0-14100> METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL  
EFFICIENCY OF A CODON

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<140> 09/900,345

<141> 2001-07-06

<150> AU PP8078

<151> 1999-01-08

<150> PCT/AU00/00008

<151> 2000-01-07

<160> 185

&lt;170&gt; PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Ala(GCA)5GFP

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle$  (1) .. (732)

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
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tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
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				85					90					95			
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Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
			115					120				125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
	145				150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165					170					175				
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
	195					200						205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
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Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
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ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ala(GCA)5GFP

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			20					25					30		



Met	Ala	Ala	Ala	Ala	Ala	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
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gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
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gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	

225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

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			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	

145	150	155	160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att				528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca				576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc				624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc				672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag				720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
	225	230	235	240
ctg tac aag tga				732
Leu Tyr Lys				

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Ala(GCG)5GFP

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20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140		
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160		
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175		
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220		
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240		
Leu Tyr Lys		

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tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	144
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	192
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	240



65	70	75	80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc				288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly				
	85	90	95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag				336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys				
	100	105	110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc				384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile				
	115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac				432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His				
	130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac				480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
	145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att				528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca				576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc				624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc				672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag				720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
	225	230	235	240
ctg tac aag tga				732
Leu Tyr Lys				
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                   35                                  40                                  45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
                   50                                  55                                  60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
                   65                                  70                                  75                                  80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                                   85                                  90                                  95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
                                   100                                  105                                  110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
                   115                                  120                                  125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
                   130                                  135                                  140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
                   145                                  150                                  155                                  160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                                   165                                  170                                  175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                   180                                  185                                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                   195                                  200                                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                   210                                  215                                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
                   225                                  230                                  235                                  240  
 Leu Tyr Lys

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<212> DNA

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<223> Description of Artificial Sequence: Arg(AGA)5GFP

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<222> (1)..(732)

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

ctg tac aag tga 732  
 Leu Tyr Lys

<210> 10  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Arg(AGA)5GFP

<400> 10  
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 11

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(AGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 11

atg agg agg agg agg agg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140

[illegible]

100	105	110
Thr Arg Ala Glu Val Lys Phe	Glu Gly Asp Thr Leu Val	Asn Arg Ile
115	120	125
Glu Leu Lys Gly Ile Asp Phe	Lys Glu Asp Gly Asn Ile	Leu Gly His
130	135	140
Lys Leu Glu Tyr Asn Tyr	Asn Ser His Asn Val	Tyr Ile Met Ala Asp
145	150	155 160
Lys Gln Lys Asn Gly Ile Lys	Val Asn Phe Lys Ile	Arg His Asn Ile
165	170	175
Glu Asp Gly Ser Val Gln Leu	Ala Asp His Tyr Gln Gln	Asn Thr Pro
180	185	190
Ile Gly Asp Gly Pro Val Leu	Leu Pro Asp Asn His Tyr	Leu Ser Thr
195	200	205
Gln Ser Ala Leu Ser Lys Asp	Pro Asn Glu Lys Arg Asp	His Met Val
210	215	220
Leu Leu Glu Phe Val Thr Ala	Ala Gly Ile Thr His Gly	Met Asp Glu
225	230	235 240
Leu Tyr Lys		

<210> 13

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 13

atg cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 14

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGA)5GFP



<400> 14

Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240  
Leu Tyr Lys

<210> 15

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 15

atg cgc cgc cgc cgc cgc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga	732
Leu Tyr Lys	

<210> 16  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Arg(CGC)5GFP

<400> 16	
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 17  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Arg(CGG)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 17  
atg cgg cgg cgg cgg cgg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 18  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Arg(CGG)5GFP

<400> 18  
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly



ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 20

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGT)5GFP

<400> 20

Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 21

<211> 732

<212> DNA

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Asn(AAC) 5GFP

<220>

<221> CDS

<222> (1) .. (732)

<400> 21

atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 22  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asn(AAC)5GFP

<400> 22

Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                   180                  185                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                   195                  200                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                   210                  215                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225                  230                  235                  240  
 Leu Tyr Lys

<210> 23  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asn(AAT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 23  
 atg aat aat aat aat aat agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Asn Asn Asn Asn Ser Lys Gly Glu Leu Phe Thr Gly Val  
   1                  5                  10                  15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                   20                  25                  30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                   35                  40                  45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
                   50                  55                  60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
                   65                  70                  75                  80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                   85                  90                  95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
                   100                  105                  110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384

Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145			150				155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230				235					240		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 24  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asn(AAT)5GFP

<400> 24  
 Met Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

65	70	75	80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	85	90	95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	100	105	110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	145	150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	165	170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235
Leu Tyr Lys			

<210> 25

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC) 5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 25

atg gac gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70				75					80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
	115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145			150				155					160			
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
		180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
	195					200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210				215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 26

<211> 243

<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC)5GFP

<400> 26

Met	Asp	Asp	Asp	Asp	Asp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65				70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	145				150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
		180						185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195						200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215						220			
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
	225				230					235					240
Leu	Tyr	Lys													

<210> 27  
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 27

atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	



180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

<210> 28  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asp(GAT)5GFP

<400> 28  
 Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                                   165                                  170                                  175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                                   180                                  185                                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                                   195                                  200                                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                                   210                                  215                                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225                                  230                                  235                                  240  
 Leu Tyr Lys

<210> 29  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Cys(TGC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 29  
 atg tgc tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                                  5                                  10                                  15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                                   20                                  25                                  30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                                   35                                  40                                  45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
   50                                  55                                  60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
   65                                  70                                  75                                  80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                                   85                                  90                                  95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

100	105	110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

<210> 30

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGC)5GFP

<400> 30

Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
---

50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145				150					155						160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165					170						175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195					200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225				230					235						240

Leu Tyr Lys

<210> 31

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 31

atg	tgt	tgt	tgt	tgt	tgt	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Cys	Cys	Cys	Cys	Cys	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10						15		

gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	

20							25					30					
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
		50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
		65					70					75			80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
				100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
				115					120					125			
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
				130					135					140			
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
						150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
						165					170					175	
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
						180					185					190	
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
								200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
								215					220				
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
								230					235			240	
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 32  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys (TGT) 5GFP

<400> 32

Met	Cys	Cys	Cys	Cys	Cys	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	1	5	10	15
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	20	25	30	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	35	40	45	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	50	55	60	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	65	70	75	80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	85	90	95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	100	105	110	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	115	120	125	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	130	135	140	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	145	150	155	160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	165	170	175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	180	185	190	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	195	200	205	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	210	215	220	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	225	230	235	240
Leu	Tyr	Lys																	

<210> 33  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gln(CAA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

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<400> 33
atg caa caa caa caa caa agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1             5             10             15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20             25             30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35             40             45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50             55             60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
             65             70             75             80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85             90             95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
             145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att  528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165             170             175

```

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 34  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gln(CAA)5GFP

<400> 34

Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	



Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 35  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gln(CAG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 35  
 atg cag cag cag cag cag agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 36

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gln(CAG)5GFP

<400> 36

Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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35	40	45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr		
50	55	60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro		
65	70	75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly		
	85	90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys		
	100	105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile		
	115	120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
	130	135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
	145	150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
	225	230 235 240

Leu Tyr Lys

<210> 37

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 37

atg gaa gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga  
 Leu Tyr Lys

732

<210> 38  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Glu(GAA)5GFP

<400> 38  
 Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                  5                  10                  15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                   20                  25                  30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
           35                  40                  45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
   50                  55                  60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
   65                  70                  75                  80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
           85                  90                  95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
           100                  105                  110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
   115                  120                  125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
   130                  135                  140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
  145                  150                  155                  160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
           165                  170                  175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
   180                  185                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
   195                  200                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
   210                  215                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
  225                  230                  235                  240

Leu Tyr Lys

<210> 39

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 39

atg gag gag gag gag gag agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 40  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Glu(GAG)5GFP

<400> 40  
 Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 41

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 41

atg gga gga gga gga gga agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80



gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 42

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGA)5GFP

<400> 42

Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe



atg ggc ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

ctg tac aag tga  
 Leu Tyr Lys

732

<210> 44  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGC)5GFP

<400> 44  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 45

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 45

atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480

Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145						150				155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235					240		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 46

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGG)5GFP

<400> 46

Met	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25				30				
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85						90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 47  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 47  
 atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85						90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100						105					110		
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120						125			
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185						190		
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200						205			
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 48  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGT)5GFP

<400> 48  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val



1	5	10	15
Val	Pro	Ile	Leu
20		25	30
Val	Glu	Leu	Asp
Ser	Val	Ser	Gly
35		40	45
Glu	Gly	Glu	Gly
Leu	Lys	Phe	Ile
50		55	60
Cys	Thr	Thr	Gly
Leu	Val	Thr	Thr
65		70	75
Phe	Ser	Tyr	Gly
Asp	His	Met	Lys
		85	90
Gln	His	Asp	Phe
Tyr	Val	Gln	Glu
		100	105
Arg	Thr	Ile	Phe
Thr	Arg	Ala	Glu
		115	120
Val	Lys	Phe	Glu
Glu	Leu	Lys	Gly
Ile	Asp	Phe	Lys
		135	140
Val	Gln	Leu	Ala
Lys	Leu	Glu	Tyr
145		150	155
Asn	Tyr	Asn	Ser
Lys	Gln	Lys	Asn
		165	170
Gly	Ile	Lys	Val
Glu	Asp	Gly	Ser
		180	185
Val	Gln	Leu	Ala
Ile	Gly	Asp	Gly
		195	200
Pro	Val	Leu	Leu
Gln	Ser	Ala	Leu
		210	215
Ser	Lys	Asp	Pro
Leu	Leu	Glu	Phe
225		230	235
Val	Thr	Ala	Ala
Leu	Tyr	Lys	

<210> 49

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: His(CAC)5GFP

<220>

<221> CDS

<222> (1) .. (732)

<400> 49

atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	

210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			
<210> 50			
<211> 243			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: His(CAC)5GFP			
<400> 50			
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
1	5	10	15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
20	25	30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
35	40	45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
50	55	60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
65	70	75	80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
85	90	95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
100	105	110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
115	120	125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
130	135	140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
165	170	175	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
180	185	190	
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 51

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: His(CAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 51

atg cat cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His

130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			

<210> 52

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: His(CAT)5GFP

<400> 52

Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 53  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ile(ATA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 53  
 atg ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

50	55	60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
65	70	75	80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85	90	95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100	105	110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			

<210> 54

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATA) 5GFP

<400> 54

Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 55

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATC)5GFP



<220>

<221> CDS

<222> (1)..(732)

<400> 55

atg atc atc atc atc atc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctg ctg cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
  
 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
  
 ctg tac aag tga 732  
 Leu Tyr Lys

<210> 56  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ile(ATC)5GFP

<400> 56  
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 57

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 57

atg att att att att att agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 58  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ile(ATT)5GFP

<400> 58  
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                     85                    90                    95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
                     100                    105                    110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
                     115                    120                    125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
                     130                    135                    140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145                    150                    155                    160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                     165                    170                    175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                     180                    185                    190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                     195                    200                    205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                     210                    215                    220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225                    230                    235                    240  
 Leu Tyr Lys

<210> 59  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(CTA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 59  
 atg cta cta cta cta cta agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                    5                    10                    15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                     20                    25                    30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                     35                    40                    45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 60

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTA)5GFP

<400> 60

Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 61

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 61

atg	ctc	ctc	ctc	ctc	ctc	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10				15				

gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
		20						25				30				

tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	

gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85					90					95			

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			

acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				

gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					

aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150					155					160		

aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170					175			

gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
		180						185					190			



atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 62  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(CTC)5GFP

<400> 62

Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 63  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Leu(CTG) 5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 63  
atg ctg ctg ctg ctg ctg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 64  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(CTG)5GFP

<400> 64  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 65

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 65

atg ctt ctt ctt ctt ctt agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 66

<211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5GFP

<400> 66

Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165					170						175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
		180						185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195					200						205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 67

<211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 67

atg tta tta tta tta tta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180	185
190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195	200
205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210	215
220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225	230
235	240
ctg tac aag tga	732
Leu Tyr Lys	

<210> 68  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(TTA)5GFP

<400> 68  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160



Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 69  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 69  
 atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 70  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(TTG) 5GFP

<400> 70  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 71  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 71  
 atg aaa aaa aaa aaa agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96

Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr		Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
130						135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200						205			
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 72  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<400> 72  
 Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                  5                  10                  15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                   20                  25                  30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
           35                  40                  45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
       50                  55                  60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
   65                  70                  75                  80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                   85                  90                  95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
           100                  105                  110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
       115                  120                  125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
   130                  135                  140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
  145                  150                  155                  160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
           165                  170                  175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
           180                  185                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
   195                  200                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
   210                  215                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
  225                  230                  235                  240  
 Leu Tyr Lys

<210> 73  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAG) 5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

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<400> 73
atg aag aag aag aag aag agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1             5             10             15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20             25             30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35             40             45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50             55             60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
             65             70             75             80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85             90             95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100            105            110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115            120            125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130            135            140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
             145            150            155            160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att  528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile

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165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

<210> 74

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Lys(AAG)5GFP

<400> 74

Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 75

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(TTT) 5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 75

atg ttt ttt ttt ttt ttt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	



85					90					95						
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 76

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(TTT) 5GFP

<400> 76

Met	Phe	Phe	Phe	Phe	Phe	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1					5				10					15	

Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		



1	5	10	15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96			
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe				
20 25 30				
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144			
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr				
35 40 45				
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192			
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr				
50 55 60				
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240			
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro				
65 70 75 80				
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288			
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly				
85 90 95				
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336			
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys				
100 105 110				
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384			
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile				
115 120 125				
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432			
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His				
130 135 140				
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480			
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
145 150 155 160				
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528			
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
165 170 175				
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576			
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
180 185 190				
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624			
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
195 200 205				
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672			
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
210 215 220				
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720			
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
225 230 235 240				

ctg tac aag tga  
Leu Tyr Lys

732

<210> 78  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Phe(TTC)5GFP

<400> 78  
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

240

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<210> 79
<211> 732
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Pro(CCC)5GFP

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<220>
<221> CDS
<222> (1) .. (732)
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xciii

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 80  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pro(CCC)5GFP

<400> 80	
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 81

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 81

atg ccg ccg ccg ccg ccg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 82

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCG)5GFP

<400> 82

Met	Pro	Pro	Pro	Pro	Pro	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1															
					5					10				15	



Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                   20                                  25                                  30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                   35                                  40                                  45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
                   50                                  55                                  60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
                   65                                  70                                  75                                  80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                   85                                  90                                  95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
                   100                                  105                                  110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
                   115                                  120                                  125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
                   130                                  135                                  140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
                   145                                  150                                  155                                  160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                   165                                  170                                  175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                   180                                  185                                  190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                   195                                  200                                  205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                   210                                  215                                  220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
                   225                                  230                                  235                                  240  
 Leu Tyr Lys

<210> 83

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 83

atg cct cct cct cct cct agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

ctg tac aag tga 732  
 Leu Tyr Lys

<210> 84  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pro(CCT)5GFP

<400> 84  
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235 240

Leu Tyr Lys

<210> 85  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pro(CGA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 85	
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Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 86  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pro(CGA)5GFP

<400> 86  
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 87  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 87  
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Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 88

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(AGC)5GFP

<400> 88

Met	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5						10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
		20						25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90						95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
		180						185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
	195						200					205				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
Leu	Tyr	Lys														

<210> 89

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(AGT)5GFP

<220>



<221> CDS

<222> (1) .. (732)

<400> 89

atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672

Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
210						215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235					240		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 90  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(AGT)5GFP

<400> 90

Met	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1					5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
	115						120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150						155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
	180							185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	

195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235 240
Leu Tyr Lys		

<210> 91  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 91  
 atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432

Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
130						135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185						190		
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 92  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCA)5GFP

<400> 92															
Met	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 93

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 93

atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
50							55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70				75						80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aac	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
	115						120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145					150					155					160		
aag	caa	aag	aac	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165					170						175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
		180						185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
	195						200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230				235						240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 94

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCC)5GFP

<400> 94

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Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1              5              10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
      20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
      85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100              105              110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115              120              125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130              135              140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145              150              155              160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165              170              175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180              185              190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195              200              205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210              215              220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225              230              235              240

Leu Tyr Lys
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<210> 95

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCG) 5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 95

atg tcg tcg tcg tcg tcg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	



195	200	205	
cag tct gcc ctg tct aaa gat	ccc aac gaa aag aga gac cac atg gtc	672	
Gln Ser Ala Leu Ser Lys Asp	Pro Asn Glu Lys Arg Asp His Met Val		
210	215 220		
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720		
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230 235 240		
ctg tac aag tga	732		
Leu Tyr Lys			

<210> 96  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCG)5GFP

<400> 96  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

180	185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235
240		
Leu Tyr Lys		

<210> 97  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCT) 5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 97  
 atg tct tct tct tct tct agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			

<210> 98  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCT)5GFP

<400> 98  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
                     85                                    90                                    95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
                     100                                    105                                    110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
                     115                                    120                                    125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
                     130                                    135                                    140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145                                    150                                    155                                    160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                     165                                    170                                    175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                     180                                    185                                    190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                     195                                    200                                    205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                     210                                    215                                    220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225                                    230                                    235                                    240  
 Leu Tyr Lys

<210> 99  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thr(ACA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 99  
 atg aca aca aca aca aca agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                    5                                    10                                    15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                     20                                    25                                    30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

35	40	45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca			192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
50	55	60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
65	70	75	80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85	90	95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100	105	110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			

<210> 100  
 <211> 243  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACA) 5GFP

<400> 100

Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240  
Leu Tyr Lys

<210> 101

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACC) 5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 101

atg acc acc acc acc acc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 102  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thr(ACC)5GFP

<400> 102

Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	



				165					170					175					
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro				
			180					185					190						
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr				
		195					200					205							
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val				
	210					215					220								
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu				
225					230					235					240				
Leu	Tyr	Lys																	

<210> 103  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thr(ACG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 103																
atg	acg	acg	acg	acg	acg	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Thr	Thr	Thr	Thr	Thr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5				10				15				
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt																96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25				30				
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc																144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca																192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca																240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75					80		
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc																288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85					90					95			
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag																336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105				110				

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 104  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thr(ACG)5GFP

<400> 104  
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 105

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 105

atg act act act act act agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 106  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<400> 106

Met	Thr	Thr	Thr	Thr	Thr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1					5				10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
		20						25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
			85						90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
		180						185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195						200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 107  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trp(TGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 107

atg tgg tgg tgg tgg tgg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 108  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trp(TGG)5GFP

<400> 108

Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	

145		150		155		160									
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165					170						175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240

Leu Tyr Lys

<210> 109

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 109

atg	tat	tat	tat	tat	tat	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Tyr	Tyr	Tyr	Tyr	Tyr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1					5				10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			85					90						95		



tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 110

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<400> 110

Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 111

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 111

atg tac tac tac tac tac agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732

Leu Tyr Lys

<210> 112

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<400> 112

Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 113

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 113

atg gta gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
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Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 114  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Val(GTA)5GFP

<400> 114

Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
			85						90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His

130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
145	150	155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
	225	230 235 240

Leu Tyr Lys

<210> 115

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 115

atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
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Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
			115				120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
	145				150				155						160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165					170					175				
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
	195					200						205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210				215						220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
	225				230				235						240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 116  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Val(GTC)5GFP

<400>	116																
Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5					10					15			
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				





Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	

225	230	235	240	
ctg tac aag tga				732
Leu Tyr Lys				

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<210> 118
<211> 243
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Val(GTG)5GFP

<400> 118															
Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 119  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Val(GTT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 119  
 atg gtt gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

145	150	155	160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att				528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca				576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc				624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc				672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag				720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235	240
ctg tac aag tga				732
Leu Tyr Lys				

<210> 120

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTT)5GFP

<400> 120

Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140		
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160		
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175		
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220		
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240		
Leu Tyr Lys		

<210> 121

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TAA) 5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 121

atg taa taa taa taa taa agc aag ggc gag gaa ctg ttc act ggc gtg Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10	48
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 15 20 25	96
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 30 35 40	144
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 45 50 55	192
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240



<222> (1) .. (732)

<400> 122

atg tag tag tag tag tag agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
15 20 25	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
30 35 40	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
45 50 55	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
60 65 70 75	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
80 85 90	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
95 100 105	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
110 115 120	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
125 130 135	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
140 145 150 155	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
160 165 170	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
175 180 185	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
190 195 200	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672



Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
205						210					215					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
220					225				230					235		
ctg	tac	aag	tga													732
Leu	Tyr	Lys														
<210> 123																
<211> 732																
<212> DNA																
<213> Artificial Sequence																
<220>																
<223> Description of Artificial Sequence: Stop(TGA) 5GFP																
<220>																
<221> CDS																
<222> (1)..(732)																
<400> 123																
atg	tga	tga	tga	tga	tga	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met						Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1								5						10		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			15					20					25			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		30				35						40				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	45					50					55					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
60					65				70					75		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
			80						85					90		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		95						100					105			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		110					115					120				

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
125 130 135	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
140 145 150 155	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
160 165 170	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
175 180 185	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
190 195 200	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
205 210 215	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
220 225 230 235	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 124  
 <211> 717  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: GFP humanized control

<220>  
 <221> CDS  
 <222> (1)..(717)

<400> 124	
atg agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg	48
Met Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggt gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct	624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg	672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	
210 215 220	
acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga	717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

<210> 125

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GFP humanized

control

<400> 125

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1           5           10           15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20           25           30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
          35           40           45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
          50           55           60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65           70           75           80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85           90           95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100          105          110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
          115          120          125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
          130          135          140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
          145          150          155          160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
          165          170          175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
          180          185          190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
          195          200          205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
          210          215          220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
          225          230          235

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<210> 126

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ala(GCA)5  
primer

<400> 126  
cggggtacca tggcagcagc agcagcaagc aagggcgagg aactgttcac tggc 54

<210> 127  
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<220>  
<223> Description of Artificial Sequence: Ala(GCC)5  
primer

<400> 127  
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<210> 128  
<211> 54  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ala(GCG)5  
primer

<400> 128  
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<210> 129  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ala(GCT)5  
primer

<400> 129  
cggggtacca tggctgctgc tgctgctagc aagggcgagg aactgttcac tggc 54

<210> 130  
<211> 54  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Arg(AGA)5  
primer

<400> 130  
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<210> 131  
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 <223> Description of Artificial Sequence: Arg(AGG)5  
       primer  
  
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 <210> 132  
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 <223> Description of Artificial Sequence: Arg(CGA)5  
       primer  
  
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       primer  
  
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 <223> Description of Artificial Sequence: Arg(CGG)5  
       primer  
  
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 <210> 135  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: arg(CGT)5  
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<400> 135  
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<210> 136  
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<220>  
 <223> Description of Artificial Sequence: Asn(AAC)5  
 primer

<400> 136  
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<210> 137  
 <211> 54  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Asn(AAT)5  
 primer

<400> 137  
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<210> 138  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asp(GAC)5  
 primer

<400> 138  
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<210> 139  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Asp(GAT)5  
 primer

<400> 139

cggggtacca tggatgatga tgatgatagc aagggcgagg aactgttcac tggc 54

<210> 140

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGC)5  
primer

<400> 140

cggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc 54

<210> 141

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGT)5  
primer

<400> 141

cggggtacca tgtgttggtg ttgttgtagc aagggcgagg aactgttcac tggc 54

<210> 142

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gln(CAA)5  
primer

<400> 142

cggggtacca tgcaacaaca acaacaaagc aagggcgagg aactgttcac tggc 54

<210> 143

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gln(CAG)5  
primer

<400> 143

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<210> 144

<211> 54



<212> DNA  
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 <223> Description of Artificial Sequence: Glu(GAA)5  
       primer  
  
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 <210> 145  
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 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Glu(GAG)5  
       primer  
  
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 <210> 146  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Gly(GGA)5  
       primer  
  
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 <210> 147  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Gly(GGC)5  
       primer  
  
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 <210> 148  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Gly(GGG)5

primer

<400> 148  
cggggtacca tggggggggg gggggggagc aagggcgagg aactgttcac tggc 54

<210> 149  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Gly(GGT)5  
primer

<400> 149  
cggggtacca tgggtggtgg tggtagtagc aagggcgagg aactgttcac tggc 54

<210> 150  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: His(CAC)5  
primer

<400> 150  
cggggtacca tgcaccacca ccaccacagc aagggcgagg aactgttcac tggc 54

<210> 151  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: His(CAT)5  
primer

<400> 151  
cggggtacca tgcacatca tcatcatagc aagggcgagg aactgttcac tggc 54

<210> 152  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ile(ATA)5  
primer

<400> 152  
cggggtacca tgataataat aataataagc aagggcgagg aactgttcac tggc 54

<210> 153  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ile(ATC) 5  
       primer  
  
 <400> 153  
 cggggtacca tgatcatcat catcatcagc aagggcgagg aactgttcac tggc 54  
  
 <210> 154  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ile(ATT) 5  
       primer  
  
 <400> 154  
 cggggtacca tgattattat tattattagc aagggcgagg aactgttcac tggc 54  
  
 <210> 155  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Leu(CTA) 5  
       primer  
  
 <400> 155  
 cggggtacca tgctactact actactaagc aagggcgagg aactgttcac tggc 54  
  
 <210> 156  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Leu(CTC) 5  
       primer  
  
 <400> 156  
 cggggtacca tgctcctcct cctcctcagc aagggcgagg aactgttcac tggc 54  
  
 <210> 157  
 <211> 54  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Leu(CTG)5  
 primer

<400> 157  
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<210> 158  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(CTT)5  
 primer

<400> 158  
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<210> 159  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(TTA)5  
 primer

<400> 159  
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<210> 160  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Leu(TTG)5  
 primer

<400> 160  
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<210> 161  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAA)5  
 primer

<400> 161  
 cggggtacca tgaaaaaaaa aaaaaaagc aagggcgagg aactgttcac tggc 54

<210> 162  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAG) 5  
 primer

<400> 162  
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<210> 163  
 <211> 54  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Phe(CTT) 5  
 primer

<400> 163  
 cggggtacca tgctttcttct tcttcttagc aagggcgagg aactgttcac tggc 54

<210> 164  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Phe(TTC) 5  
 primer

<400> 164  
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<210> 165  
 <211> 54  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Pro(CCC) 5  
 primer

<400> 165  
 cggggtacca tgcccccccc cccccccagc aagggcgagg aactgttcac tggc 54

<210> 166

<211> 54  
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 <220>  
 <223> Description of Artificial Sequence: Pro(CCG)5  
       primer  
  
 <400> 166  
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 <210> 167  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Pro(CCT)5  
       primer  
  
 <400> 167  
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 <210> 168  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Pro(CGA)5  
       primer  
  
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 <210> 169  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Ser(AGC)5  
       primer  
  
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 cggggtacca tgagcagcag cagcagcagc aagggcgagg aactgttcac tggc 54  
  
 <210> 170  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Description of Artificial Sequence: Ser(AGT)5  
primer

<400> 170  
cggggtacca tgagtagtag tagtagtagc aagggcgagg aactgttcac tggc 54

<210> 171  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ser(TCA)5  
primer

<400> 171  
cggggtacca tgtcatcatc atcatcaagc aagggcgagg aactgttcac tggc 54

<210> 172  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ser(TCC)5  
primer

<400> 172  
cggggtacca tgtcctcctc ctctccagc aagggcgagg aactgttcac tggc 54

<210> 173  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ser(TCG)5  
primer

<400> 173  
cggggtacca tgctgctgct gctgctgagc aagggcgagg aactgttcac tggc 54

<210> 174  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ser(TCT)5  
primer

<400> 174  
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<210> 175  
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 <223> Description of Artificial Sequence: Thr(ACA) 5  
       primer  
  
 <400> 175  
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 <210> 176  
 <211> 54  
 <212> DNA  
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 <223> Description of Artificial Sequence: Thr(ACC) 5  
       primer  
  
 <400> 176  
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 <210> 177  
 <211> 54  
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 <223> Description of Artificial Sequence: Thr(ACG) 5  
       primer  
  
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 <210> 178  
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 <220>  
 <223> Description of Artificial Sequence: Thr(ACT) 5  
       primer  
  
 <400> 178  
 cggggtacca tgactactac tactactagc aagggcgagg aactgttcac tggc 54  
  
 <210> 179  
 <211> 54  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trp(TGG)5  
primer

<400> 179

cggggtacca tgtggtggtg gtggtggagc aagggcgagg aactgttcac tggc 54

<210> 180

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5  
primer

<400> 180

cggggtacca tgtattatta ttattatagc aagggcgagg aactgttcac tggc 54

<210> 181

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTA)5  
primer

<400> 181

cggggtacca tggtagtagt agtagtaagc aagggcgagg aactgttcac tggc 54

<210> 182

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTC)5  
primer

<400> 182

cggggtacca tggtcgtcgt cgtcgtcagc aagggcgagg aactgttcac tggc 54

<210> 183

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val( GTG)5  
primer

<400> 183  
cggggtacca tgggtggtggt ggtggtgagc aagggcgagg aactgttcac tggc 54

<210> 184  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Val(GTT)5  
primer

<400> 184  
cggggtacca tgggtggtggt tgggtgtagc aagggcgagg aactgttcac tggc 54

<210> 185  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 3'  
oligonucleotide common primer

<400> 185  
ccggaattct cacttgtagc ggtggtccat gcc 33